```
gggagtcgac ccacgcgtcc ggtagcctgg tgctctttct c atg gct tca ccc agc 56
                                              Met Ala Ser Pro Ser
                                                1               5

ctc ccg ggc agt gac tgc tcc caa atc att gat cac agt cat gtc ccc 104
Leu Pro Gly Ser Asp Cys Ser Gln Ile Ile Asp His Ser His Val Pro
            10                  15                  20

gag ttt gag gtg gcc acc tgg atc aaa atc acc ctt att ctg gtg tac 152
Glu Phe Glu Val Ala Thr Trp Ile Lys Ile Thr Leu Ile Leu Val Tyr
        25                  30                  35

ctg atc atc ttc gtg atg ggc ctt ctg ggg aac agc gcc acc att cgg 200
Leu Ile Ile Phe Val Met Gly Leu Leu Gly Asn Ser Ala Thr Ile Arg
    40                  45                  50

gtc acc cag gtg ctg cag aag aaa gga tac ttg cag aag gag gtg aca 248
Val Thr Gln Val Leu Gln Lys Lys Gly Tyr Leu Gln Lys Glu Val Thr
55                  60                  65

gac cac atg gtg agt ttg gct tgc tcg gac atc ttg gtg ttc ctc atc 296
Asp His Met Val Ser Leu Ala Cys Ser Asp Ile Leu Val Phe Leu Ile
70                  75                  80                  85

ggc atg ccc atg gag ttc tac agc atc atc tgg aat ccc ctg acc acg 344
Gly Met Pro Met Glu Phe Tyr Ser Ile Ile Trp Asn Pro Leu Thr Thr
                90                  95                  100

tcc agc tac acc ctg tcc tgc aag ctg cac act ttc ctc ttc gag gcc 392
Ser Ser Tyr Thr Leu Ser Cys Lys Leu His Thr Phe Leu Phe Glu Ala
            105                 110                 115

tgc agc tac gct acg ctg ctg cac gtg ctg aca ctc agc ttt gag cgc 440
Cys Ser Tyr Ala Thr Leu Leu His Val Leu Thr Leu Ser Phe Glu Arg
        120                 125                 130

tac atc gcc atc tgt cac ccc ttc agg tac aag gct gtg tcg gga cct 488
Tyr Ile Ala Ile Cys His Pro Phe Arg Tyr Lys Ala Val Ser Gly Pro
    135                 140                 145

tgc cag gtg aag ctg ctg att ggc ttc gtc tgg gtc acc tcc gcc ctg 536
Cys Gln Val Lys Leu Leu Ile Gly Phe Val Trp Val Thr Ser Ala Leu
150                 155                 160                 165

gtg gca ctg ccc ttg ctg ttt gcc atg ggt act gag tac ccc ctg gtg 584
Val Ala Leu Pro Leu Leu Phe Ala Met Gly Thr Glu Tyr Pro Leu Val
                170                 175                 180

aac gtg ccc agc cac cgg ggt ctc act tgc aac cgc tcc agc acc cgc 632
Asn Val Pro Ser His Arg Gly Leu Thr Cys Asn Arg Ser Ser Thr Arg
            185                 190                 195

cac cac gag cag ccc gag acc tcc aat atg tcc atc tgt acc aac ctc 680
His His Glu Gln Pro Glu Thr Ser Asn Met Ser Ile Cys Thr Asn Leu
        200                 205                 210

tcc agc cgc tgg acc gtg ttc cag tcc agc atc ttc ggc gcc ttc gtg 728
Ser Ser Arg Trp Thr Val Phe Gln Ser Ser Ile Phe Gly Ala Phe Val
    215                 220                 225
```

FIGURE 1

```
gtc tac ctc gtg gtc ctg ctc tcc gta gcc ttc atg tgc tgg aac atg   776
Val Tyr Leu Val Val Leu Leu Ser Val Ala Phe Met Cys Trp Asn Met
230                 235                 240                 245

atg cag gtg ctc atg aaa agc cag aag ggc tcg ctg gcc ggg ggc acg   824
Met Gln Val Leu Met Lys Ser Gln Lys Gly Ser Leu Ala Gly Gly Thr
                250                 255                 260

cgg cct ccg cag ctg agg aag tcc gag agc gaa gag agc agg acc gcc   872
Arg Pro Pro Gln Leu Arg Lys Ser Glu Ser Glu Glu Ser Arg Thr Ala
            265                 270                 275

agg agg cag acc atc atc ttc ctg agg ctg att gtt gtg aca ttg gcc   920
Arg Arg Gln Thr Ile Ile Phe Leu Arg Leu Ile Val Val Thr Leu Ala
        280                 285                 290

gta tgc tgg atg ccc aac cag att cgg agg atc atg gct gcg gcc aaa   968
Val Cys Trp Met Pro Asn Gln Ile Arg Arg Ile Met Ala Ala Ala Lys
    295                 300                 305

ccc aag cac gac tgg acg agg tcc tac ttc cgg gcg tac atg atc ctc  1016
Pro Lys His Asp Trp Thr Arg Ser Tyr Phe Arg Ala Tyr Met Ile Leu
310                 315                 320                 325

ctc ccc ttc tcg gag acg ttt ttc tac ctc agc tcg gtc atc aac ccg  1064
Leu Pro Phe Ser Glu Thr Phe Phe Tyr Leu Ser Ser Val Ile Asn Pro
                330                 335                 340

ctc ctg tac acg gtg tcc tcg cag cag ttt cgg cgg gtg ttc gtg cag  1112
Leu Leu Tyr Thr Val Ser Ser Gln Gln Phe Arg Arg Val Phe Val Gln
            345                 350                 355

gtg ctg tgc tgc cgc ctg tcg ctg cag cac gcc aac cac gag aag cgc  1160
Val Leu Cys Cys Arg Leu Ser Leu Gln His Ala Asn His Glu Lys Arg
        360                 365                 370

ctg cgc gta cat gcg cac tcc acc acc gac agc gcc cgc ttt gtg cag  1208
Leu Arg Val His Ala His Ser Thr Thr Asp Ser Ala Arg Phe Val Gln
    375                 380                 385

cgc ccg ttg ctc ttc gcg tcc cgg cgc cag tcc tct gca agg aga act  1256
Arg Pro Leu Leu Phe Ala Ser Arg Arg Gln Ser Ser Ala Arg Arg Thr
390                 395                 400                 405

gag aag att ttc tta agc act ttt cag agc gag gcc gag ccc cag tct  1304
Glu Lys Ile Phe Leu Ser Thr Phe Gln Ser Glu Ala Glu Pro Gln Ser
                410                 415                 420

aag tcc cag tca ttg agt ctc gag tca cta gag ccc aac tca ggc gcg  1352
Lys Ser Gln Ser Leu Ser Leu Glu Ser Leu Glu Pro Asn Ser Gly Ala
            425                 430                 435

aaa cca gcc aat tct gct gca gag aat ggt ttt cag gag cat gaa gtt  1400
Lys Pro Ala Asn Ser Ala Ala Glu Asn Gly Phe Gln Glu His Glu Val
        440                 445                 450

tgaatgtcaa gcgagggagc cttgagtggg aactggccct ccagccctaa gaaaacgtca 1460

ctctcactct gcagtctcaa actatgcccc catcagggat ggaatggaca ctggaggctt 1520

tacaaaaggc agatgcccac ctcagtgact tctaaggact gactctgcca gcctggcctt 1580
```

FIGURE 1, CONT.

gactccggtt acacagacat gggggtgaac tttcactcca cctccttcct tcaagtacat 1640

actgaaaatt cagtcaagct gaatttattc agaatgcttt accgagctct ttcattattt 1700

gcacaggaac aaaagagaac acggactccc gctccctacc cagaataaaa ggacacccag 1760

aagaaactca ctcagggagg tgggggttg ggggcgaggg ctggaagaac aatgcaggag 1820

ggggtggcat ctccttcagc ttcagcagtg tgccgagaag agggctaatt tgaggaacag 1880

gatggtggtg cggagccctg gcctgagggc cgaggcagaa cttccccttt tcttgggcct 1940

tggcccgtta caaagagggg tgttgcagca gctgatgcaa actgagttca gtttccctgg 2000

ggagcagaag gactggtacc cggcagaggc gatgagacag gccgctgatg atgcacagga 2060

cttgcggtac atgatcccgg cactttgctc catcacttct ttctgacaca tgtcttgaac 2120

gttcaccgtg caattcacaa tgaactcggg ggaggagcag tcgttgttca gctggaattc 2180

ttcacactgg tagcactgga tttgcagcgc aaagccttgc ggactcccgg ggatgccccg 2240

gtgctatctt cgccttcctt cccgagcctt gcagcaggtg gtgcgggaga ccgcttgccc 2300

gccggagtgc gttggtgccc ccgcccccaa tccgcacatt cccatcccct ttccgcacat 2360

ccttagggag catccatttc cgtggaaatc gcctcctaag ctttagctcc tcttcaccct 2420

tttctccccc ggccacttct gggggcagct ctctcacgcc gggacgcaga tcatttaatt 2480

ctgcatcgcn tcngcagagc tggtctgtaa aggggcttaa atgacttt 2528

FIGURE 1, CONT.

FIGURE 2

stat 1h
stat 6h
stat 24h
LSS 1h
LSS 6h
LSS 24h
IL-1 1h
IL-1 6h
Il-1 24h
0
2
4
6
8
Stat 1hr
Stat 6hr
Stat 24hr
LSS 1hr
LSS 6hr
LSS 24hr
IL-1 1hr
IL-1 6hr
IL-1 24hr
0
2
4
6
8

FIGURE 3

SUBSTITUTE SHEET

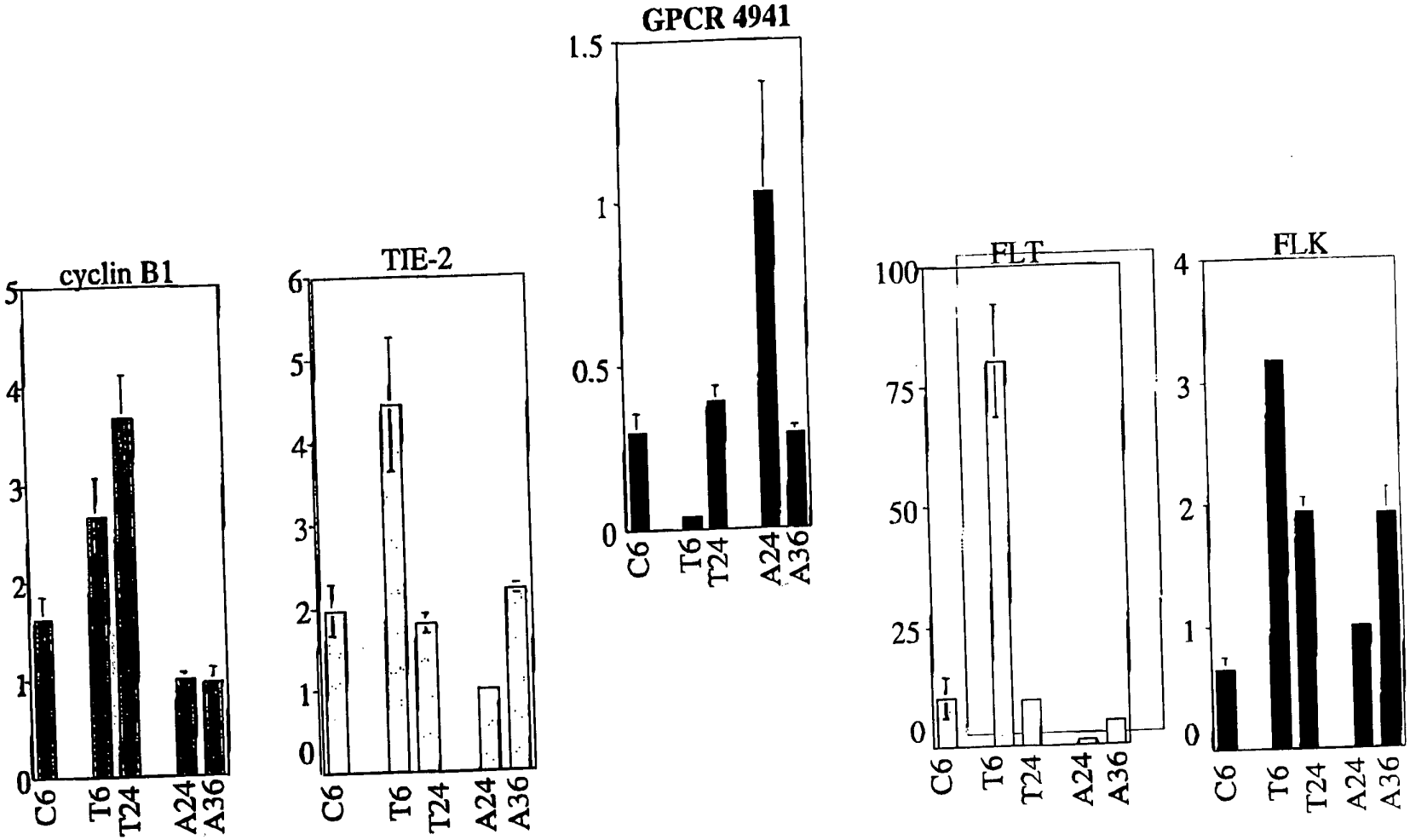
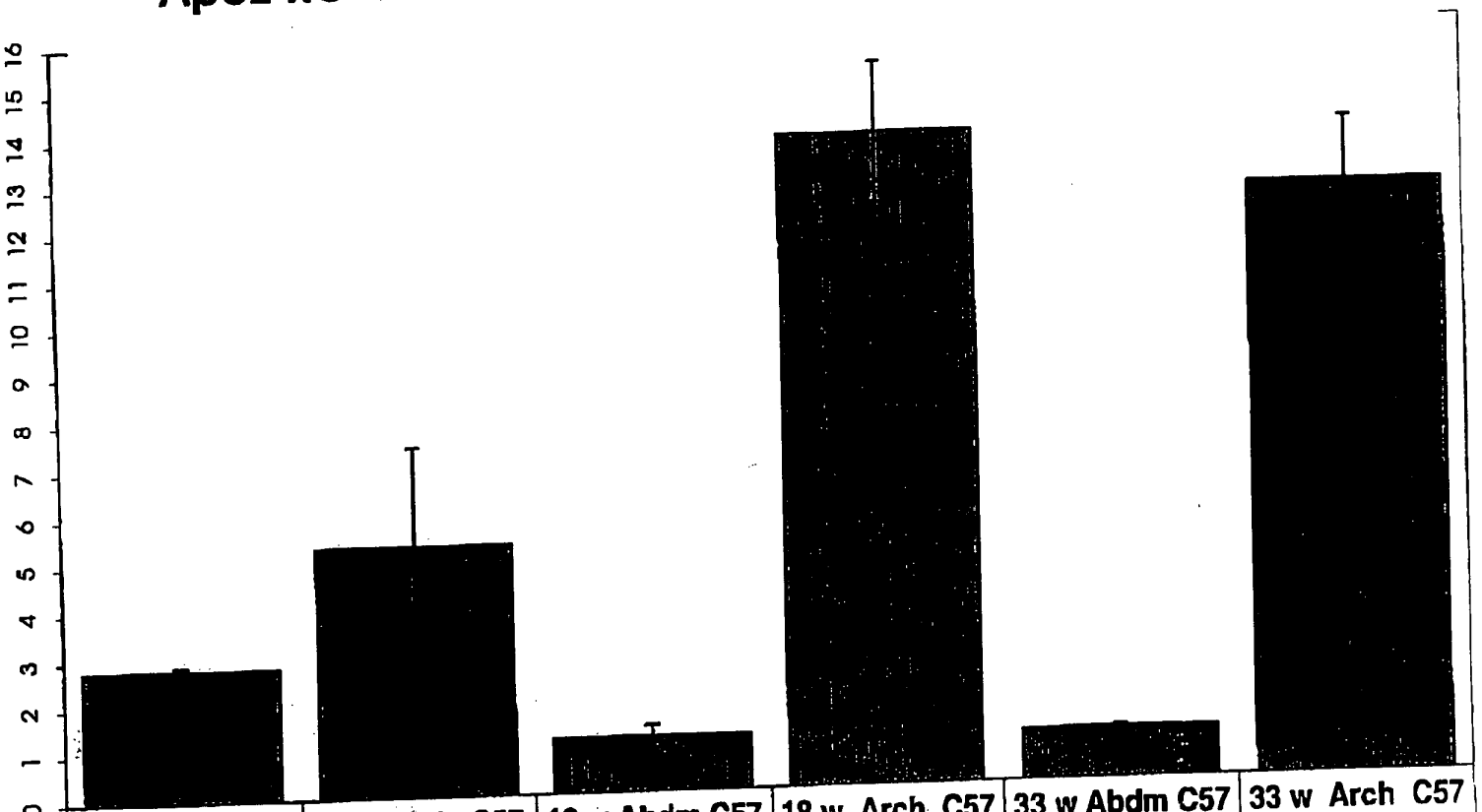


FIGURE 4

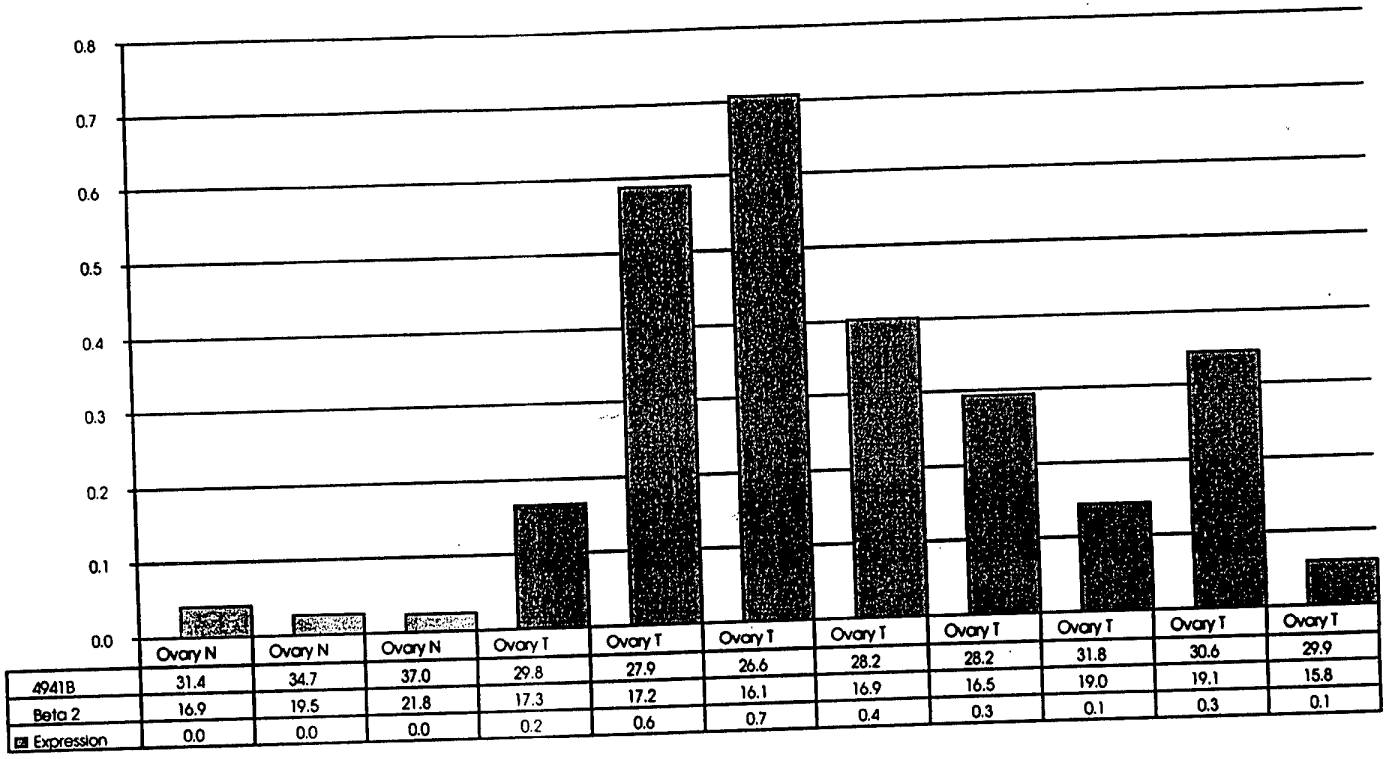
Cyclin B1
Conf HM
HM 24
C2
P5
A24
0
1
2
3
4
5
4941
Conf HM
HM 24
C2
P5
A24
0
1
2
3
4
5
6

FIGURE 5

FIGURE 9



	5 w Abdm C57	5 w Arch C57	18 w Abdm C57	18 w Arch C57	33 w Abdm C57	33 w Arch C57
4941 CT	25.55	25.44	26.94	25.75	26.67	25.51
GAPDH CT	17.03	18.24	16.95	19.46	16.83	19.3
STDEV	0.08	2.10	0.24	1.49	0.04	1.35
Mean R. E.	2.78	5.31	1.15	13.83	1.06	12.55



	Ovary N	Ovary N	Ovary N	Ovary T	Ovary T	Ovary T	Ovary T	Ovary T	Ovary T	Ovary T	Ovary T
4941B	31.4	34.7	37.0	29.8	27.9	26.6	28.2	28.2	31.8	30.6	29.9
Beta 2	16.9	19.5	21.8	17.3	17.2	16.1	16.9	16.5	19.0	19.1	15.8
Expression	0.0	0.0	0.0	0.2	0.6	0.7	0.4	0.3	0.1	0.3	0.1

FIGURE 7A

PATENT PENDING

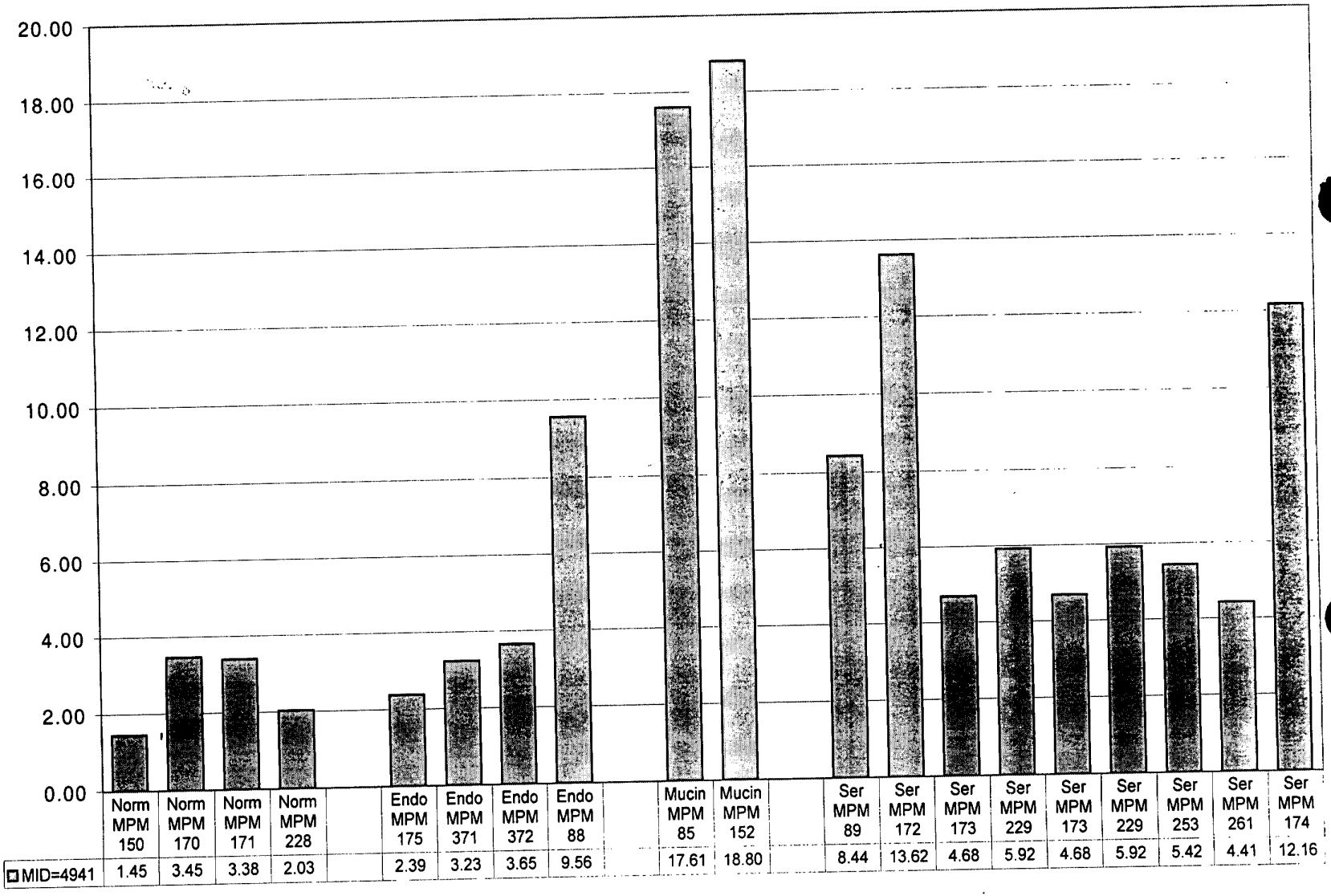
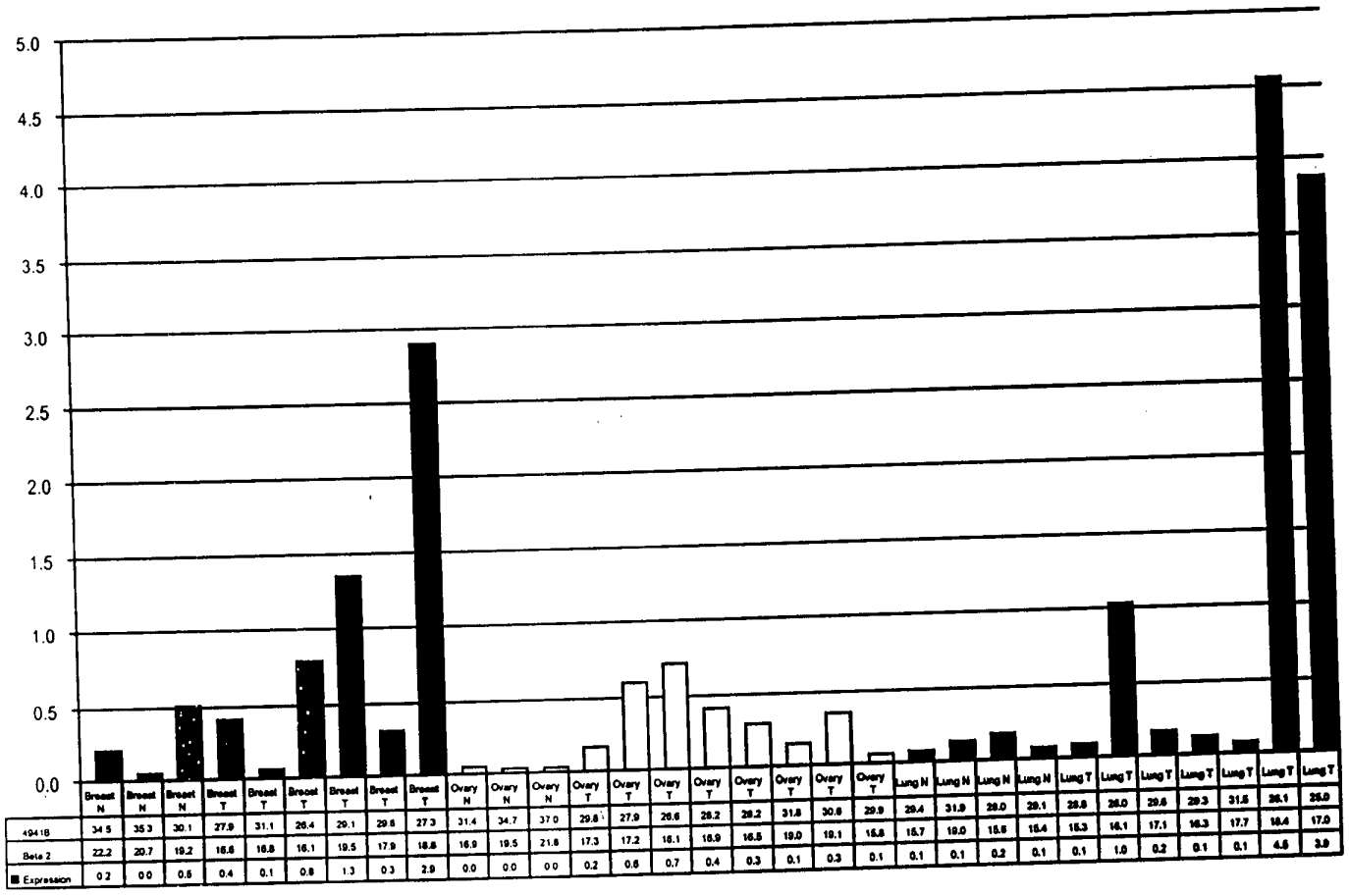


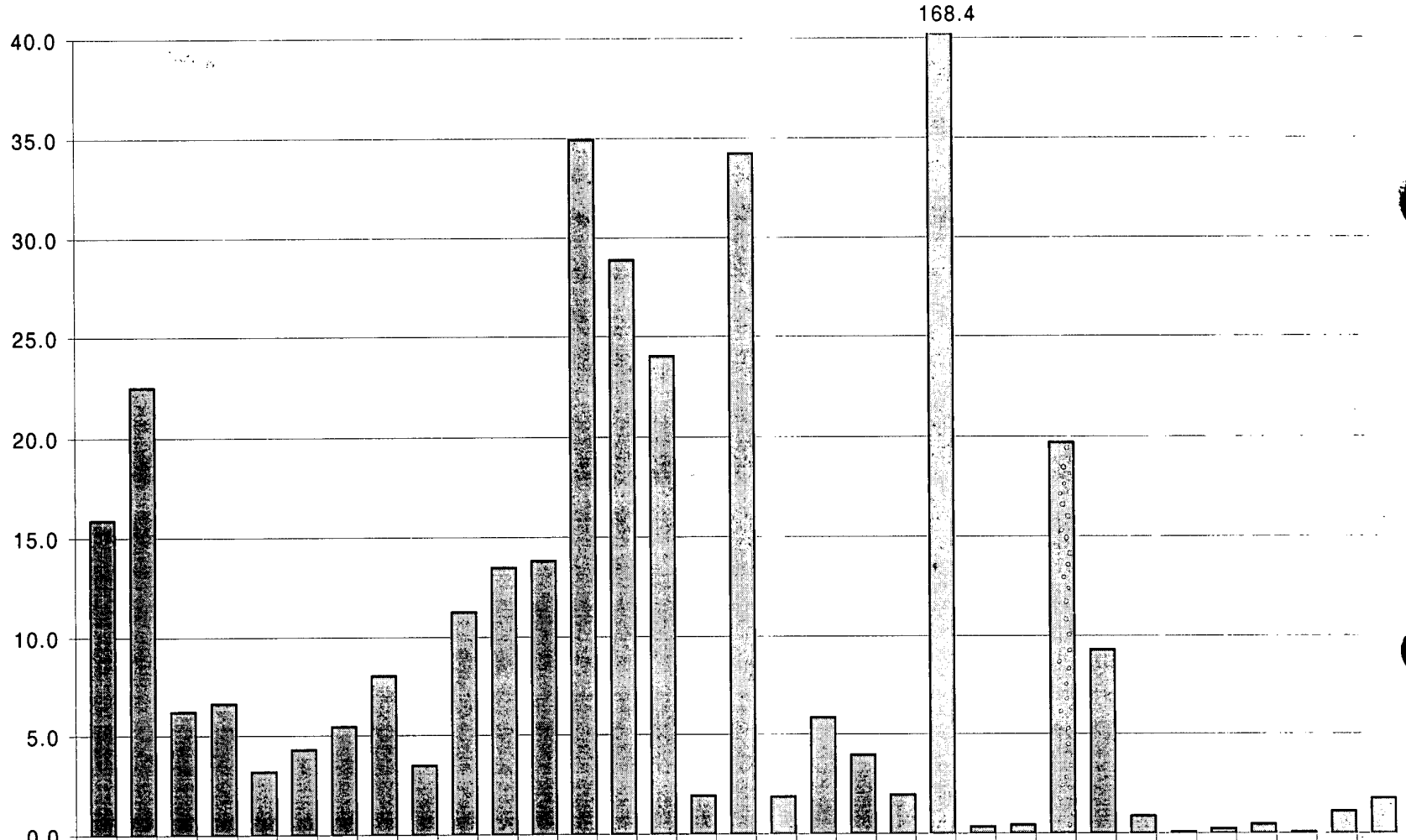
FIGURE 7 B.



	Breast N	Breast N	Breast N	Breast T	Breast T	Breast T	Breast T	Breast T	Breast T	Ovary N	Ovary N	Ovary N	Ovary T	Ovary T	Ovary T	Ovary T	Ovary T	Ovary T	Ovary T	Ovary T	Lung N	Lung N	Lung N	Lung N	Lung T	Lung T	Lung T	Lung T	Lung T	Lung T
49418	34.5	35.3	30.1	27.9	31.1	26.4	29.1	29.6	27.3	31.4	34.7	37.0	29.8	27.9	26.6	28.2	28.2	31.8	30.8	29.9	29.4	31.9	28.0	29.1	28.8	26.0	29.6	29.3	31.8	26.1	25.0
Beta 2	22.2	20.7	19.2	18.6	18.8	16.1	19.5	17.9	18.8	16.9	19.5	21.8	17.3	17.2	18.1	18.9	16.5	19.0	19.1	18.8	18.7	19.0	18.8	18.4	18.3	16.1	17.1	16.3	17.7	18.4	17.0
Expression	0.2	0.0	0.5	0.4	0.1	0.8	1.3	0.3	2.9	0.0	0.0	0.0	0.2	0.6	0.7	0.4	0.3	0.1	0.3	0.1	0.1	0.1	0.2	0.1	0.1	1.0	0.2	0.1	0.1	4.8	3.9

FIGURE 8A

FIGURE 8B



	Colon N	Colon N	Colon N	Colon T	Colon T	Colon T	Colon T	Colon T	Colon T	Colon T	Colon T	Liver Met	Liver Met	Liver Met	Liver Met	Liver Nor	Liver Nor	Brain N	Brain N	Brain N	Brain N	Astrocyt	Brain T	Brain T	Brain T	Brain T	Brain T	HMVE C-Arr	HMVE C-Prol	Placenta	Fetal Adrenal	Fetal Liver	Fetal Liver
4941B	29.0	27.2	27.9	25.2	27.9	24.0	25.7	28.5	25.5	24.9	23.5	24.4	25.1	23.8	25.9	26.0	29.3	32.6	31.0	32.5	31.8	25.0	29.1	28.0	25.2	27.0	30.3	36.1	34.4	34.8	38.2	30.4	28.5
Beta 2	23.0	21.8	20.6	18.0	19.7	16.2	18.2	21.6	17.4	18.5	17.3	18.2	20.3	18.7	20.5	16.9	24.4	23.5	23.6	24.5	22.8	22.4	17.6	16.7	19.5	20.2	20.1	21.7	22.4	23.7	23.6	20.5	19.4
Expression	15.8	22.5	6.2	6.6	3.2	4.3	5.4	8.0	3.5	11.2	13.5	13.8	34.9	28.9	24.0	1.9	34.2	1.8	5.8	4.0	1.9	168.4	0.3	0.4	19.7	9.3	0.9	0.0	0.2	0.5	0.0	1.1	1.7